

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2021.004S** |  |
| **Short title:** Create one new species in the genus *Iflavirus* (*Picornavirales*: *Iflaviridae*) | | |
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**Author(s) and email address(es)**

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**List the ICTV Study Group(s) that have seen this proposal**

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| Dicistroviridae/Iflaviridae Study Group |

**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | June 2, 2021 |
| Date of this revision (if different to above) | September 17, 2021 |

**ICTV-EC comments and response of the proposer**

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| Many thanks for submitting the three taxonomy proposals for species designation in the *Iflavivirdae*. This was reviewed at the ICTV Executive Committee meeting yesterday as it was given a designation of Ac. This means that it is accepted pending minor changes as listed below:   1. The changes in the three proposals were coded on the same spreadsheet but actually three separate spreadsheets are required, one for each proposal. So can these be separated? 2. There is a formal check done of the spreadsheet and I attach the errors detected. Can you take a look at these and correct where indicated. You don’t need to include taxonomy above the level of order so you can remove some of the errors by just deleting the higher ranks. 3. The proposed names were not in a binomial format. There is now a two year remaining period for species names to be re-formatted, and the general advice would be to ensure that any new names are compliant. However, you may want to think about the best way to do this and you might keep the proposed species names as they are pending a comprehensive renaming at a later date. 4. As an advisory note, sequences used in trees produced to support proposals are best labelled with nucleotide accession numbers rather than the derived protein accession number or virus names (although a combined label with nucleotide accession numbers and virus names is ideal). However there is no need to change this in the current proposals.   Response   1. The spreadsheets have now been split so there is one for each proposal 2. The spreadsheets have been checked and passed without errors 3. We will review species names for the whole virus family and may be in a position to rename them all in binomial format for the next round of taxonomy proposals 4. Noted |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2021.004S.R.Iflavirus\_1nsp.xlsx |

**Abstract**

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| We discovered a relatively abundant novel Iflavirus in the faeces of wild Swedish house crickets (Acheta domesticus) through RNA sequencing. RT-qPCR analyses showed that this virus is both common and abundant in faecal and insect samples from both commercially reared and wild crickets, and thus a natural part of the *A. domesticus* virome. The genomes of the commercial and wild strains of AdIV were completely req-sequenced by Sanger sequencing of RT-PCR amplicons. The 3’ terminus was obtained by amplifying with anchored oligo-dT. Phylogenetic analyses located AdIV solidly, with high confidence, in a monophyletic clade well within the Iflavirus family tree. All major genomic regions returned similar cladograms, meaning that the virus is not a construct or a recombinant of disparate virus elements. |

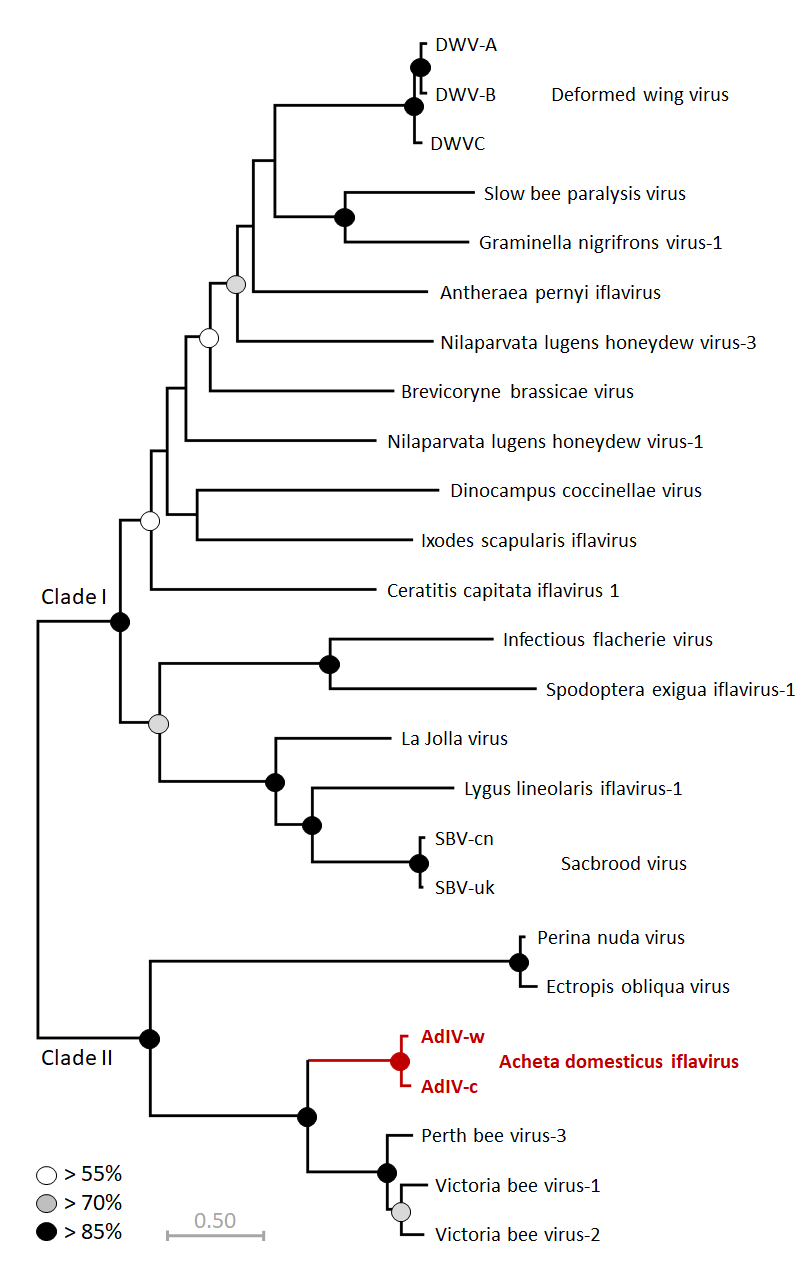
**Text of proposal**

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| |  | | --- | | **Reasons to justify the creation and assignment of the new species:**  **Reasons to justify the creation and assignment of the new species:**  Species demarcation criteria for the members of the genus *Iflavirus*   * Natural host range: species can be differentiated on the basis of their natural host range * Sequence identity between the CPs of isolates and strains of a species is above 90%.   ----------------------------------------------------------------------------------------------------------  The genome sequence of *Acheta domesticus iflavirus* (AdIV) was originally discovered in the RNA sequencing data of the faeces of the house cricket *Acheta domesticus* (de Miranda et al., 2021). A relatively high proportion of viral RNA sequencing reads were assigned to AdIV, increasing the likelihood that this was a true infectious virus of A. domesticus and not a passively acquired virus. The full genome sequences of two strains of AdIV (from wild and cultivated *A. domesticus*) were obtained through screening RNA sequencing libraries and Sanger sequencing PCR products produced with specific primers. The complete genome sequences of the two strains of AdIV (GenBank Accessions MW281483 and MW548506) shows the following features that fulfill the *Iflavirus* genus inclusion criteria:  Genome: Positive-sense, single stranded RNA genome which is at least 9050 nt long and contains a single open reading frame (ORF). The ORF encodes a polyprotein of 2817 amino acid residues flanked by approximately 552 nt of 5’-UTR and 49 nt of 3’-UTR, followed by a natural poly-A tail, a characteristic feature of Iflaviruses and other Pirconavirales. The order of the various structural and non-structural proteins encoded by the polyprotein is typical for Iflaviruses, including the highly characteristic leader protein (Lp) prior to the four structural protein units (Figure 1).  Phylogeny: Phylogenetic analysis with the amino acid sequences of the polyprotein of Iflaviruses locates AdIV in a monophyletic group within the Iflaviridae, together with other recognized Iflaviruses (Figure 2). The two strains of AdIV are about 90% identical at nucleotide level (93% at amino acid level) and about 70% identical at amino acid level to its closest relative: a clade of newly discovered Iflaviruses from honeybees in Australia (Roberts et al. 2018).  Natural host range: AdIV is thus far exclusively been detected in faecal and tissue samples of *Acheta domesticus*. No dedicated host-range studies have been conducted so far, nor has the virus been detected in a different cricket species, *Gryllus bimaculatus*.  Taxonomy proposal: We propose to assign both strains of AdIV to the new species *Acheta domesticus iflavirus* | |

**Supporting evidence**

C:\Users\jrdm\AppData\Local\Microsoft\Windows\INetCache\Content.Word\AdIV genome map.tif

**Figure. 1**: Genome organization of Acheta domesticus iflavirus (AdIV).



**Figure 2.** The polyprotein amino acid sequences of the new Acheta domesticus iflavirus were aligned to a selection of 23 related iflaviruses by CLUSTAL-W, as implemented by MEGA-X. All positions containing gaps or missing data in the multiple alignment were excluded from the phylogenetic analyses. The phylogenetic relationship between the different taxa was inferred using the Maximum Likelihood method. The statistical confidence for each branching node was determined by bootstrapping the alignment 500 times. The tree is drawn to scale and is measured in number of amino acid substitutions per site.

**References**

de Miranda JR, Granberg F, Onorati P, Jansson A, Berggren Å. Virus Prospecting in Crickets-Discovery and Strain Divergence of a Novel Iflavirus in Wild and Cultivated Acheta domesticus. Viruses. 2021 Feb 25;13(3):364. doi: 10.3390/v13030364. PMID: 33669085; PMCID: PMC7996529.

Roberts JMK, Anderson DL, Durr PA. Metagenomic analysis of Varroa-free Australian honey bees (Apis mellifera) shows a diverse Picornavirales virome. J Gen Virol. 2018 Jun;99(6):818-826. doi: 10.1099/jgv.0.001073. Epub 2018 May 11. PMID: 29749926.